

(1) GENERAL INFORMATION:



- (i) APPLICANTS: Gaugler, Béatrice; Van den Eynde, Benoît; van der Bruggen, Pierre; Boon-Falleur, Thierry
- (ii) TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: Felfe & Lynch
 (B) STREET: 805 Third Avenue
 (C) CITY: New York City
 (D) STATE: New York
 (F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 (B) COMPUTER: IBM
 (C) OPERATING SYSTEM: PC-DOS
 (D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER: 08/037,230
 (B) FILING DATE: 26-MARCH-1993
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: PCT/US92/04354
 (B) FILING DATE: 22-MAY-1992
- (viii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: 07/807,043
 (B) FILING DATE: 12-DECEMBER-1991
- (ix) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: 07/764,364
 (B) FILING DATE: 23-SEPTEMBER-1991
- (x) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: 07/728,838
 (b) FILING DATE: 9-JULY-1991
- (xi) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: 07/705,702
 (B) FILING DATE: 23-MAY-1991
- (xii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Hanson, Norman D.
 (B) REGISTRATION NUMBER: 30,946
 (C) REFERENCE/DOCKET NUMBER: LUD 253.5
- (xiii) TELECOMMUNICATION INFORMATION:
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- (2) INFORMATION FOR SEQUENCE ID NO: 1:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 462 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60
 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT 120
 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTCGA AGTTCCGCCT ACAGCTCTAG 180
 CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240
 CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG CATGCATTGT 360
 GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT 420
 TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC 462

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(2) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs.

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT 48
 Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
 5 10 15
 GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA 96
 Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
 20 25 30
 GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA 144
 Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
 35 40 45
 AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG 192
 Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
 50 55 60
 TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC 240
 Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
 65 70 75 80
 TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC 288
 Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
 85 90 95
 GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 336
 Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
 100 105 110
 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG 384
 Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
 115 120 125
 GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG 432
 Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
 130 135 140
 GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG 480
 Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
 145 150 155 160
 AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC 528
 Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
 165 170 175
 CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT 576
 Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
 180 185 190
 GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG 624
 Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu
 195 200 210
 GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 672
 Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
 220 225 230 235
 TAG 675

- (2) INFORMATION FOR SEQUENCE ID NO: 3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT 60
TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT 120
TCATTATGCA AAGATGTCAC SAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC 180
ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC 228

- (2) INFORMATION FOR SEQUENCE ID NO: 4:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1365 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50
 GAAGATCGTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100
 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
 AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200
 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG 350
 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
 ACCCTTTGTG CC 462
 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756
 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT 924
 GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT 966
 TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG 1008
 AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT 1050
 GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG 1092
 GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 1134
 TAG 1137
 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG 1187
 TTGTTTTTTT TTCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA 1237
 ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT 1287
 CTGACTGCAT GGTGAACCTT CATATGATAC ATAGGATTAC ACTTGACCT 1337
 GTTAAAAATA AAAGTTTGAC TTGCATAC 1365

- (2) INFORMATION FOR SEQUENCE ID NO: 5:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4698 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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ACCACAGGAG	AATGAAAAGA	ACCCGGGACT	CCCAAAGACG	CTAGATGTGT	50
GAAGATCTTG	ATCACTCATT	GGGTGTCTGA	GTTCTGCGAT	ATTCATCCCT	100
CAGCCAATGA	GCTTACTGTT	CTCGTGGGGG	GTTTGTGAGC	CTTGGGTAGG	150
AAGTTTTGCA	AGTTCCGCCT	ACAGCTCTAG	CTTGTGAATT	TGTACCCTTT	200
CACGTAAAAA	AGTAGTCCAG	AGTTTACTAC	ACCCTCCCTC	CCCCCTCCCA	250
CCTCGTGCTG	TGCTGAGTTT	AGAAGTCTTC	CTTATAGAAG	TCTTCCGTAT	300
AGAACTCTTC	CGGAGGAAGG	AGGGAGGACC	CCCCCCTTTT	GCTCTCCCG	350
CATGCATTGT	GTCAACGCCA	TTGCACTGAG	CTGGTCTGAAG	AAGTAAGCCG	400
CTAGCTTGCG	ACTCTACTCT	TATCTTAACT	TAGCTCGGCT	TCCTGCTGGT	450
ACCCTTTGTG	CC				462
ATG TCT GAT	AAC AAG AAA CCA GAC	AAA GCC CAC	AGT GGC TCA		504
GGT GGT GAC	GGT GAT GGG AAT AGG	TGC AAT TTA	TTG CAC CGG		546
TAC TCC CTG	GAA GAA ATT CTG	CCT TAT CTA	GGG TGG CTG	GTC	588
TTC GCT GTT	GTC ACA AGT TTT	CTG GCG CTC	CAG ATG TTC		630
ATA GAC GCC	CTT TAT GAG GAG	CAG TAT GAA	AGG GAT GTG	GCC	672
TGG ATA GCC	AGG CAA AGC AAG	CGC ATG TCC	TCT GTC	GAT GAG	714
GAT GAA GAC	GAT GAG GAT GAT	GAG GAT GAC	TAC TAC	GAC GAC	756
GAG GAC GAC	GAC GAC GAT GCC	TTC TAT GAT	GAT GAT	GAT GAT	798
GAG GAA GAA	GAA TTT GAG AAC	CTG ATG GAT	GAT GAA	TCA GAA	840
GAT GAG GCC	GAA GAA GAG	ATG AGC GTG	GAA ATG	GGT GCC	882
GCT GAG GAA	ATG GGT GCT	GGC GCT AAC	TGT GCC	T	916
GTGAGTAACC	CGTGGTCTTT	ACTCTAGATT	CAGGTGGGGT	GCATTCTTTA	966
CTCTTGCCCC	CATCTGTAGT	AAAGACCACA	TTTGGTTGG	GGGTCATTGC	1016
TGGAGCCATT	CCTGGCTCTC	CTGTCCACGC	CTATCCCCGC	TCCTCCCATC	1066
CCCCACTCCT	TGCTCCGCTC	TCCTTCTCTT	TCCCACCTTG	CCTCTGGAGC	1116
TTCAGTCCAT	CCTGCTCTGC	TCCCTTTCCC	CTTGCTCTC	CTTGCTCCCC	1166
TCCCCCTCGG	CTCAACTTTT	CGTCCCTTCT	GCTCTCTGAT	CCCCACCCTC	1216
TTCAGGCTTC	CCCATTGCT	CCTCTCCCCG	AACCCTCCCC	TTCCTGTTCC	1266
CCTTTTCGCG	CCTTTTCTTT	CCTGCTCCCC	TCCCCCTCCC	TATTTACCTT	1316
TCACCAGCTT	TGCTCTCCCT	GCTCCCCCTC	CCCTTTTGCA	CCTTTTCTTT	1366
TCCTGCTCCC	CTCCCCCTCC	CCTCCCTGTT	TACCCTTCAC	CGCTTTTCCT	1416
CTACCTGCTT	CCCTCCCCCT	TGCTGCTCCC	TCCCTATTG	CATTTTCGGG	1466
TGCTCCTCCC	TCCCCCTCCC	CCTCCCTCCC	TATTTGCATT	TTCGGGTGCT	1516
CCTCCCTCCC	CCTCCCCAGG	CCTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	1566
TTGGTTTTTC	GAGACAGGGT	TTCTCTTTGT	ATCCCTGGCT	GTCCTGGCAC	1616
TCACTCTGTA	GACCAGGCTG	GCCTCAAAC	GAGAAATCTG	CCTGCCTCTG	1666
CCTCCCAAAT	GCTGGGATTA	AAGGCTTGCA	CCAGGACTGC	CCCAGTGCAG	1716
GCCTTTCTTT	TTTCTCCTCT	CTGGTCTCCC	TAATCCCTTT	TCTGCATGTT	1766
AACTCCCTTT	TTGGCACCTT	TCCTTTACAG	GACCCCTCC	CCCTCCCTGT	1816
TTCCCTTCCG	GCACCCTTCC	TAGCCCTGCT	CTGTTCCCTC	TCCCTGCTCC	1866
CCTCCCCCTC	TTTGCTCGAC	TTTTAGCAGC	CTTAGCTCTC	CCTGCTTTCT	1916
GCCCCGTTCC	CCTTTTTTGT	GCCTTTCCCT	CTGGCTCCCC	TCCACCTTCC	1966
AGCTCACCTT	TTTGTGTTGT	TGGTTGTTTG	GTTGTTTGGT	TTGCTTTTTT	2016
TTTTTTTTTT	GCACCTTGTT	TTCCAAGATC	CCCCTCCCCC	TCCGGCTTCC	2066
CCTCTGTGTG	CCTTTCTCTG	TCCCTCCCCC	TCGCTGGGTC	CCCCTCCCTT	2116
TCTGCCTTTC	CTGTCCCTGC	TCCCTTCTCT	GCTAACCTTT	TAATGCCTTT	2166
CTTTTCTAGA	CTCCCCCTTC	CAGGCTTGCT	GTTTGCTTCT	GTGCACTTTT	2216
CCTGACCCTG	CTCCCTTCC	CCTCCGACT	CCCCCTCTTT	TTCCACCTC	2266
CCTTTCTCCA	GCCTGTCACC	CCTCCTTCTC	TCCTCTCTGT	TTCTCCCACT	2316
TCCTGCTTCC	TTTACCCCTT	CCCTCTCCCT	ACTCTCCTCC	CTGCCTGCTG	2366
GAATTCCCTCT	CCAGCCGCCC	AGTTCCCTGC	AGTCCTGGAG	TCTTTCCTGC	2416
CTCTCTGTCC	ATCACTTCCC	CCTAGTTTCA	CTTCCCTTTC	ACTCTCCCTT	2466
ATGTGTCTCT	CTTCCCTATCT	ATCCCTTCC	TTCTGTCCCC	TCTCTCTGT	2516
CCATCACCTC	TCTCCTCCCT	TCCCTTTTCT	CTCTCTTCCA	TTTTCTTCCA	2566
CCTGCTTCTT	TACCCTGCCT	CTCCCATTC	CCTCTTACCT	TTATGCCCAT	2616
TCCATGTCCC	CTCTCAATTC	CCTGTCCCAT	TGTGCTCCCT	CACATCTTCC	2666

ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCCC 2716
 TTCCCTTTGC TTCTCCCTTC TCCTTTCCCC TTCCCTATG CCCTCTACTC 2766
 TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTGCC 2816
 CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC 2866
 ATCAACAACA AGGAGGCAAG AAACAGAGCA AAATCCCCAA ATCAGCAGGA 2916
 AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG GAATCTAGCC 2966
 AAGTGGCTCC TATAACCCTA AGTACCAAGG GAGAAAGTGA TGGTGAAGTT 3016
 CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT TTCTCAAATG 3066
 CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA 3116
 GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA AATTAGCACG 3166
 TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA 3216
 TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTAA 3266
 GGCTAAAGAT ACTTGAACCC ATAGAAGCGT TGTTAAAATA CTGCTTTCTT 3316
 TTGCTAAAAT ATTCTTTCTC ACATATTTCAT ATTCTCCAG 3355
 GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT 3396
 AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT 3438
 ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA 3480
 AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA 3522
 GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC 3564
 TTC TCA CCT TAG 3576
 GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA TATGCCTGTA 3626
 GCTAAGAGCA TCTTTTAAA AATATTATT GGTAAACTAA ACAATTGTGA 3676
 TCTTTTACA TTAATAAGTA TTAATTAAAT CCAGTATACA GTTTTAAGAA 3726
 CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT 3776
 GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA 3826
 GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG 3876
 TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT 3926
 TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCTG 3976
 TTCTGATTTT TTTCATTCTT AGACCTGTGG TTTTAAAGAG ATGAAAATCT 4026
 CTTAAAATTT CCTTCATCTT TAATTTTCTT TAACTTTAGT TTTTTCCTACT 4076
 TAGAATTCAA TTCAAATTCT TAATTCATC TTAATTTTAA GATTTCTTAA 4126
 AATGTTTTTT AAAAAAATG CAAATCTCAT TTTTAAAGAG TGAAAGCAGA 4176
 GTAAGTGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA 4226
 GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAACC AGGCCCTTGC 4276
 CAGTAGGTTA GTGAGGTGA TATGATCAGA TTATGGACAC TCTCCAATC 4326
 ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT 4376
 ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA 4426
 AGTCAGGAGT GTATTCTAAT AAGTGTGCT TATCTCTTAT TTCTTCTAC 4476
 AGTTGCAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT 4526
 TTTTTCCTC TTTTCTAATT TTCTAGTTT TAGTAATCCA GAAATTTGA 4576
 TTTTGTCTA AAGTTTCTTA TGCAAAGATG TCACCAACAG ACTTCTGACT 4626
 GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTAAA 4676
 AATAAAGTT TGACTTGCAT AC 4698

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- (2) INFORMATION FOR SEQUENCE ID NO: 6:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu Val Phe

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- (2) INFORMATION FOR SEQUENCE ID NO: 7:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2418 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG 50
 GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC 100
 TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG 150
 GGCCCGTGGA TTCTCTTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT 200
 TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT 250
 GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA 300
 CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCACT 350
 CCTGTAGAAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC 400
 TTCCTCCTTC AGGTTTTCAG GGGACAGGCC AACCAGAGG ACAGGATTCC 450
 CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTTG 500
 TTAGAGTCTC CAAGGTTTCA TTCTCAGCTG AGGCCTCTCA CACTCTCCCT 550
 CTCTCCCCAG GCCTGTGGGT CTTTATTGCC CAGCTCCTGC CCACACTCCT 600
 GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC 650
 ACTGCAAGCC TGAGGAAGCC CTTGAGGCCA AACAAGAGGC CCTGGGCCTG 700
 GTGTGTGTGC AGGCTGCCAC CTCTCTCTCC TCTCCTCTGG TCCTGGGCAC 750
 CCTGGAGGAG GTGCCCCACT CTGGGTCAAC AGATCCTCCC CAGAGTCCTC 800
 AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA 850
 CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG 900
 TATCCTGGAG TCCTTGTTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT 950
 TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG 1000
 GCAGAAATGC TGGAGAGTGT CATCAAAAT TACAAGCACT GTTTTCCTGA 1050
 GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG 1100
 TGAAGGAAGC AGACCCACCC GGCCACTCCT ATGTCTTTGT CACCTGCCTA 1150
 GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC 1200
 AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GCGGGCCATG 1250
 CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT 1300
 GGGAGGGGAG ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA 1350
 TTTGGTGACG GAAAAGTACC TGGAGTACGG CAGGTGCCCG ACAGTGATCC 1400
 CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT 1450
 ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAGTGCAAG AGTTCGCTTT 1500
 TTCTTCCCAT CCTGCGTGA AGCAGCTTTG AGAGAGGAGG AAGAGGGAGT 1550
 CTGAGCATGA GTTGCAGCCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC 1600
 ACCTTCCAGG GCCGCGTCCA GCAGCTTCCC CTGCCTCGTG TGACATGAGG 1650
 CCCATTCTTC ACTCTGAAGA GAGCGGTCAG TGTCTCTAGT AGTAGGTTTC 1700
 TGTTCTATTG GGTGACTTGG AGATTTATCT TTGTTCTCTT TTGGAATTGT 1750
 TCAAATGTTT TTTTAAAGG GATGGTTGAA TGAACCTCAG CATCCAAGTT 1800
 TATGAATGAC AGCAGTCACA CAGTTCTGTG TATATAGTTT AAGGGTAAGA 1850
 GTCTTGTTGT TTATTTCAGT TGGGAAATCC ATTCTATTTT GTGAATTGGG 1900
 ATAATAACAG CAGTGAATA AGTACTTAGA AATGTGAAAA ATGAGCAGTA 1950
 AAATAGATGA GATAAAGAAC TAAAGAAAT AAGAGATAGT CAATTCTTGC 2000
 CTTATACCTC AGTCTATTCT GTAAAATTTT TAAAGATATA TGCATACCTG 2050
 GATTTCTCTG GCTTCTTTGA GAATGTAAGA GAAATTAAAT CTGAATAAAG 2100
 AATTCTTCCT GTTCACTGGC TCTTTTCTTC TCCATGCACT GAGCATCTGC 2150
 TTTTGGGAAG GCCCTGGGTT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT 2200
 CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG 2250
 AGGTGGCAAG ATGTCTCTA AAGATGTAGG GAAAAGTGAG AGAGGGGTGA 2300
 GGGTGTGGGG CTCGGGTGA GAGTGGTGGA GTGTCAATGC CCTGAGCTGG 2350
 GGCATTTTGG GCTTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT 2400
 AATGATCTTG GGTGGATCC 2418

- (2) INFORMATION FOR SEQUENCE ID NO: 8:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5724 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-1 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CCCCGGGGCACC CACTGGCATC CCTCCCCCTA CCACCCCCAA TCCCTCCCTT 50
 TACGCCACCC ATCCAAACAT CTTCACGCTC ACCCCCAGCC CAAGCCAGGC 100
 AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCAG 150
 ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTTT 200
 CGGTCTGAGG GGGCGCTTGA GATCGGTGGA GGAAGCGGG CCCAGCTCTG 250
 TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCCC 300
 AGATAGAGGA CCCAAAATAA TCCCTTCATG CCAGTCTTGG ACCATCTGGT 350
 GGTGGACTTC TCAGGCTGGG CCACCCCCAG CCCCCTTGCT GCTTAAACCA 400
 CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAGG GCTGCTTAGG 450
 AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG 500
 AGGGCTGAGG GTCCCTAAGA CCCCCTCCC GTGACCCAAC CCCCCTCCA 550
 ATGCTCACTC CCGTGACCCA ACCCCCTCTT CATGTGCATT CCAACCCCCA 600
 CCCCACATCC CCCCACCCAT CCCTCAACCC TGATGCCCAT CCGCCCAGCC 650
 ATTCCACCCT CACCCCCACC CCCCACCCCA CGCCCCTCC CACCCCCACC 700
 CAGGCAGGAT CCGGTTCCCG CCAGGAAACA TCCGGGTGCC CGGATGTGAC 750
 GCCACTGACT TGCGCATTGT GGGGCAGAGA GAAGCGAGGT TTCCATTCTG 800
 AGGGACGGCG TAGAGTTCGG CCGAAGGAAC CTGACCCAGG CTCTGTGAGG 850
 AGGCAAGGTG AGAGGCTGAG GGAGGACTGA GGACCCCGCC ACTCCAAATA 900
 GAGAGCCCCA AATATTCCAG CCGCGCCCTT GCTGCCAGCC CTGGCCCCACC 950
 CGCGGGAAGA CGTCTCAGCC TGGGCTGCCC CCAGACCCTT GCTCCAAAAG 1000
 CCTTGAGAGA CACCAGGTTT TTCTCCCCAA GCTCTGGAAT CAGAGGTTGC 1050
 TGTGACCAGG GCAGGACTGG TTAGGAGAGG GCAGGGCACA GGCTCTGCCA 1100
 GGCATCAAGA TCAGCACCCA AGAGGGAGGG CTGTGGGCCC CCAAGACTGC 1150
 ACTCCAATCC CCACTCCAC CCCATTGCA TTCCCATTC CCACCCAACC 1200
 CCCATCTCCT CAGCTACACC TCCACCCCA TCCCTACTCC TACTCCGTCA 1250
 CCTGACCACC ACCCTCCAGC CCCAGCACCA GCCCAACCC TTCTGCCACC 1300
 TCACCCTCAC TGCCCCAAC CCCCACCTCA TCTCTCTCAT GTGCCCCACT 1350
 CCCATCGCCT CCCCCATTCT GGCAGAATCC GGTGTTGCCCC TGCTCTCAAC 1400
 CCAGGGAAGC CCTGGTAGGC CCGATGTGAA ACCACTGACT TGAACCTCAC 1450
 AGATCTGAGA GAAGCCAGGT TCATTTAATG GTTCTGAGGG GCGGCTTGAG 1500
 ATCCAATGAG GGGAGTGGTT TTAGGCTCTG TGAGGAGGCA AGGTGAGATG 1550
 CTGAGGGAGG ACTGAGGAGG CACACACCCC AGGTAGATGG CCCCAAAATG 1600
 ATCCAGTACC ACCCTGCTG CCAGCCCTGG ACCACCCGGC CAGGACAGAT 1650
 GTCTCAGCTG GACCACCCCC CGTCCCGTCC CACTGCCACT TAACCCACAG 1700
 GGCAATCTGT AGTCATAGCT TATGTGACCG GGGCAGGTT GGTCAAGAGA 1750
 GGCAGGGCCC AGGCATCAAG GTCCAGCATC CGCCCCGCAT TAGGGTCAGG 1800
 ACCCTGGGAG GGAAGTGAAG GTTCCCCACC CACACCTGTC TCCTCATCTC 1850
 CACCGCCACC CCACTCACAT TCCCATACCT ACCCCCTACC CCAACCTCA 1900
 TCTTGTCAGA ATCCCTGCTG TCAACCCACG GAAGCCACGG GAATGGCGGC 1950
 CAGGCACTCG GATCTTGACG TCCCCATCCA GGGTCTGATG GAGGGAAGGG 2000
 GCTTGAACAG GGCCCTCAGGG GAGCAGAGGG AGGGCCCTAC TGCGAGATGA 2050
 GGGAGGCCTC AGAGGACCCA GCACCCTAGG ACACCGCACC CCTGTCTGAG 2100
 ACTGAGGCTG CCACTTCTGG CCTCAAGAAT CAGAACGATG GGGACTCAGA 2150
 TTGCATGGGG GTGGGACCCA GGCCTGCAAG GCTTACGCGG AGGAAGAGGA 2200
 GGGAGGACTC AGGGGACCTT GGAATCCAGA TCAGTGTGGA CCTCGGCCCT 2250
 GAGAGGTCCA GGGCACGGTG GCCACATATG GCCCATATTT CCTGCATCTT 2300
 TGAGGTGACA GGACAGAGCT GTGGTCTGAG AAGTGGGGCC TCAGGTCAAC 2350
 AGAGGGAGGA GTTCCAGGAT CCATATGGCC CAAGATGTGC CCCCTTCATG 2400
 AGGACTGGGG ATATCCCCGG CTCAGAAAGA AGGGACTCCA CACAGTCTGG 2450
 CTGTCCCTT TTAGTAGCTC TAGGGGGACC AGATCAGGGA TGGCGGTATG 2500
 TTCCATTCTC ACTTGTAACA CAGGCAGGAA GTTGGGGGGC CCTCAGGGAG 2550
 ATGGGGTCTT GGGGTAAAGG GGGGATGTCT ACTCATGTCA GGGAAATTGG 2600
 GGTGAGGAA GCACAGGCGC TGGCAGGAAT AAAGATGAGT GAGACAGACA 2650
 AGGCTATTGG AATCCACACC CCAGAACCAA AGGGGTCAGC CCTGGACACC 2700

TCACCCAGGA TGTGGCTTCT TTTTCACTCC TGTTCACAGA TCTGGGGCAG 2750
 GTGAGGACCT CATTCTCAGA GGGTGACTCA GGTCAACGTA GGGACCCCCA 2800
 TCTGGTCTAA AGACAGAGCG GTCCCAGGAT CTGCCATGCG TTCGGGTGAG 2850
 GAACATGAGG GAGGACTGAG GGTACCCAGG GACCAGAACA CTGAGGGAGA 2900
 CTGCACAGAA ATCAGCCCTG CCCCTGCTGT CACCCACAGAG AGCATGGGCT 2950
 GGGCGCTCTG CCGAGGTCCT TCCGTTATCC TGGGATCATT GATGTCAGGG 3000
 ACGGGGAGGC CTTGGTCTGA GAAGGCTGCG CTCAGGTCAG TAGAGGGAGC 3050
 GTCCCAGGCC CTGCCAGGAG TCAAGGTGAG GACCAAGCGG GCACCTCACC 3150
 CAGGACACAT TAATTCCAAT GAATTTTGAT ATCTCTTGCT GCCCTTCCCC 3200
 AAGGACCTAG GCACGTGTGG CCAGATGTTT GTCCCTCCT GTCTTCCAT 3250
 TCCTTATCAT GGATGTGAAC TCTTGATTG GATTTCTCAG ACCAGCAAAA 3300
 GGGCAGGATC CAGGCCCTGC CAGGAAAAAT ATAAGGGCCC TGCCTGAGAA 3350
 CAGAGGGGGT CATCCACTGC ATGAGAGTGG GGATGTCACA GAGTCCAGCC 3400
 CACCCTCCTG GTAGCACTGA GAAGCCAGGG CTGTGCTTGC GGTCTGCACC 3450
 CTGAGGGCCC GTGGATTCTT CTTCTCTGGAG CTCAGGAAC CAGGCAGTGA 3500
 GGCCTTGGTC TGAGACAGTA TCCTCAGGTC ACAGAGCAGA GGATGCACAG 3550
 GGTGTGGCAG CAGTGAATGT TTGCCCTGAA TGCACACCAA GGGCCCCACC 3600
 TGCCACAGGA CACATAGGAC TCCACAGAGT CTGGCCTCAC CTCCCTACTG 3650
 TCAGTCCTGT AGAATCGACC TCTGCTGGCC GGCTGTACCC TGAGTACCCT 3700
 CTCACCTTCT CTTTCAGGTT TTCAGGGGAC AGGCCAACCC AGAGGACAGG 3750
 ATTCCCTGGA GGCCACAGAG GAGCACCAAG GAGAAGATCT GTAAGTAGGC 3800
 CTTTGTTAGA GTCTCCAAGG TTCAGTTCTC AGCTGAGGCC TCTCACACAC 3850
 TCCCTCTCTC CCCAGGCCTG TGGGTCTTCA TTGCCCAGCT CCTGCCACAA 3900
 CTCCTGCCTG CTGCCCTGAC GAGAGTCATC 3930
 ATG TCT CTT GAG CAG AGG AGT CTG CAC TGC AAG CCT GAG GAA 3972
 GCC CTT GAG GCC CAA CAA GAG GCC CTG GGC CTG GTG TGT GTG 4014
 CAG GCT GCC ACC TCC TCC TCC TCT CCT CTG GTC CTG GGC ACC 4056
 CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT CCT CCC CAG 4098
 AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC ATC AAC TTC 4140
 ACT CGA CAG AGG CAA CAC AGT GAG GGT TCC AGC AGC CGT GAA 4182
 GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG GAG TCC TTG TTC 4224
 CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG GTT GGT TTT 4266
 CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC ACA AAG GCA 4308
 GAA ATG CTG GAG AGT GTC ATC AAA AAT TAC AAG CAC TGT TTT 4350
 CCT GAG ATC TTC GGC AAA GGC TCT GAG TCC TTG CAG CTG GTC 4392
 TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC GGC CAC TCC 4434
 TAT GTC CTT GTC ACC TGC CTA GGT CTC TCC TAT GAT GGC CTG 4476
 CTG GGT GAT AAT CAG ATC ATG CCC AAG ACA GGC TTC CTG ATA 4518
 ATT GTC CTG GTC ATG ATT GCA ATG GAG GGC CAT GCT CCT 4560
 GAG GAG GAA ATC TGG GAG GAG CTG AGT GTG ATG GAG GTG TAT 4602
 GAT GGG AGG GAG CAC AGT GCC TAT GGG GAG CCC AGG AAG CTG 4644
 CTC ACC CAA GAT TTG GTG CAG GAA AAG TAC CTG GAG TAC GGC 4686
 AGG TGC CGG ACA GTG ATC CCG CAC GCT ATG AGT TCC TGT GGG 4728
 GTC CAA GGG CCC TCG CTG AAA CCA GCT ATG TGA 4761
 AAGTCCTTGA GTATGTGATC AAGGTCAGTG CAAGAGTTC 4800
 GCTTTTTCTT CCCATCCCTG CGTGAAGCAG CTTTGAGAGA GGAGGAAGAG 4850
 GGAGTCTGAG CATGAGTTGC AGCCAAGGCC AGTGGGAGGG GGACTGGGCC 4900
 AGTGCACCTT CCAGGGCCGC GTCCAGCAGC TTCCCTGCCC TCGTGTGACA 4950
 TGAGGCCCCAT TCTTCACTCT GAAGAGAGCG GTCAGTGTTC TCAGTAGTAG 5000
 GTTTCTGTTC TATTGGGTGA CTTGGAGATT TATCTTTGTT CTCTTTTGGA 5050
 ATTGTTCAAA TGTTTTTTTT TAAGGGATGG TTGAATGAAC TTCAGCATCC 5100
 AAGTTTATGA ATGACAGCAG TCACACAGTT CTGTGTATAT AGTTTAAGGG 5150
 TAAGAGTCTT GTGTTTTATT CAGATTGGGA AATCCATTCT ATTTTGTGAA 5200
 TTGGGATAAT AACAGCAGTG GAATAAGTAC TTAGAAATGT GAAAAATGAG 5250
 CAGTAAATA GATGAGATAA AGAAGTAAAG AAATTAAGAG ATAGTCAATT 5300
 CTTGCCTTAT ACCTCAGTCT ATTCTGTAAA ATTTTAAAG ATATATGCAT 5350
 ACCTGGATTT CTTGGCTTC TTTGAGAATG TAAGAGAAAT TAAATCTGAA 5400
 TAAAGAATTC TTCCTGTTCA CTGGCTCTTT TCTTCTCCAT GCACTGAGCA 5450
 TCTGCTTTTT GGAAGGCCCT GGGTTAGTAG TGGAGATGCT AAGGTAAGCC 5500
 AGACTCATAC CCACCCATAG GGTCGTAGAG TCTAGGAGCT GCAGTACCT 5550
 AATCGAGGTG GCAAGATGTC CTCTAAAGAT GTAGGGAAAA GTGAGAGAGG 5600
 GGTGAGGGTG TGGGGCTCCG GGTGAGAGTG GTGGAGTGTC AATGCCCTGA 5650
 GCTGGGGCAT TTTGGGCTTT GGGAAACTGC AGTTCCTTCT GGGGGAGCTG 5700
 ATTGTAATGA TCTTGGGTGG ATCC 5724

- (2) INFORMATION FOR SEQUENCE ID NO: 9:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4157 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-2 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Sub D.1

C1

CCCATCCAGA	TCCCCATCCG	GGCAGAATCC	GGTTCCACCC	TTGCCGTGAA	50
CCCAGGGAAG	TCACGGGGCC	GGATGTGACG	CCACTGACTT	GCACATTGGA	100
GGTCAGAGGA	CAGCGAGATT	CTCGCCCTGA	GCAACGGCCT	GACGTGGCG	150
GAGGGAAGCA	GGCGCAGGCT	CCGTGAGGAG	GCAAGGTAAG	ACGCCGAGGG	200
AGGACTGAGG	CGGGCCTCAC	CCCAGACAGA	GGGCCCCCAA	TTAATCCAGC	250
GCTGCCTCTG	CTGCCGGGCC	TGGACCACCC	TGCAGGGGAA	GACTTCTCAG	300
GCTCAGTCGC	CACCACCTCA	CCCCGCCACC	CCCCGCCGCT	TTAACCGCAG	350
GGAACCTCTGG	CGTAAGAGCT	TTGTGTGACC	AGGGCAGGGC	TGGTTAGAAG	400
TGCTCAGGGC	CCAGACTCAG	CCAGGAATCA	AGGTCAGGAC	CCCAAGAGGG	450
GACTGAGGGC	AACCCACCCC	CTACCCTCAC	TACCAATCCC	ATCCCCAAC	500
ACCAACCCCC	CCCCATCCC	TCAAACACCA	ACCCACCCC	CAAACCCAT	550
TCCCATCTCC	TCCCCACCA	CCATCCTGGC	AGAATCCGGC	TTTGCCCTG	600
CAATCAACCC	ACGGAAGCTC	CGGGAATGGC	GGCCAAGCAC	GCGGATCCTG	650
ACGTTACAT	GTACGGCTAA	GGGAGGGAAG	GGGTTGGGTC	TCGTGAGTAT	700
GGCCTTTGGG	ATGCAGAGGA	AGGGCCCAGG	CCTCCTGGAA	GACAGTGGAG	750
TCCTTAGGGG	ACCCAGCATG	CCAGGACAGG	GGGCCCCTG	TACCCCTGTC	800
TCAAACCTGAG	CCACCTTTTG	ATTCAGCCGA	GGGAATCCTA	GGGATGCAGA	850
CCCACTTCAG	GGGGTTGGGG	CCCAGCCTGC	GAGGAGTCAA	GGGGAGGAAG	900
AAGAGGGAGG	ACTGAGGGGA	CCTTGGAGTC	CAGATCAGTG	GCAACCTTGG	950
GCTGGGGGAT	CCTGGGCACA	GTGGCCGAAT	GTGCCCCGTG	CTCATTGCAC	1000
CTTCAGGGTG	ACAGAGAGTT	GAGGGCTGTG	GTCTGAGGCG	TGGGACTTCA	1050
GGTCAGCAGA	GGGAGGAATC	CCAGGATCTG	CCGACCCCAA	GGTGTGCCCC	1100
CTTCATGAGG	ACTCCCCATA	CCCCCGGCCC	AGAAAGAAGG	GATGCCACAG	1150
AGTCTGGAAG	TAAATTGTTC	TGAGCTCTGG	GGGAACCTGA	TCAGGGATGG	1200
CCCTAAGTGA	CAATCTCATT	TGTACACAG	GCAGGAGGTT	GGGGAACCCCT	1250
CAGGGAGATA	AGGTGTTGGT	GTAAGAGGA	GCTGTCTGCT	CATTTCAGGG	1300
GGTCCCCCT	TGAGAAAGGG	CAGTCCCTGG	CAGGAGTAAA	GATGAGTAAC	1350
CCACAGGAGG	CCATCATAAC	GTTCAACCTA	GAACCAAAGG	GGTCAGCCCT	1400
GGACAACGCA	CGTGGGGTAA	CAGGATGTGG	CCCCTCCTCA	CTTGCTTTTC	1450
CAGATCTCAG	GGAGTTGATG	ACCTTGTTTT	CAGAAGGTGA	CTCAGTCAAC	1500
ACAGGGGCCC	CTCTGGTCGA	CAGATGCAGT	GGTCTAGGA	TCTGCCAAGC	1550
ATCCAGGTGG	AGAGCCTGAG	GTAGGATTGA	GGGTACCCCT	GGGCCAGAAT	1600
GCAGCAAGGG	GGCCCCATAG	AAATCTGCCC	TGCCCCCTGCG	GTTACTTCAG	1650
AGACCCTGGG	CAGGGCTGTC	AGCTGAAGTC	CCCTCATTAT	CTGGGATCTT	1700
TGATGTCAGG	GAAGGGGAGG	CCTTGGTCTG	AAGGGGCTGG	AGTCAGGTCA	1750
GTAGAGGGAG	GGTCTCAGGC	CCTGCCAGGA	GTGGACGTGA	GGACCAAGCG	1800
GACTCGTCAC	CCAGGACACC	TGGACTCCAA	TGAATTGAC	ATCTCTCGTT	1850
GTCCTTCGCG	GAGGACCTGG	TCACGTATGG	CCAGATGTGG	GTCCCCCTCTA	1900
TCTCCTTCTG	TACCATATCA	GGGATGTGAG	TTCTTGACAT	GAGAGATTCT	1950
CAAGCCAGCA	AAAGGGTGGG	ATTAGGCCCT	ACAAGGAGAA	AGGTGAGGGC	2000
CCTGAGTGAG	CACAGAGGGG	ACCCTCCACC	CAAGTAGAGT	GGGGACCTCA	2050
CGGAGTCTGG	CCAACCCTGC	TGAGACTTCT	GGGAATCCGT	GGCTGTGCTT	2100
GCAGTCTGCA	CACTGAAGGC	CCGTGCATTC	CTCTCCCAGG	AATCAGGAGC	2150
TCCAGGAACC	AGGCAGTGAG	GCCTTGGTCT	GAGTCAGTGC	CTCAGGTCAC	2200
AGAGCAGAGG	GGACGCAGAC	AGTGCCAACA	CTGAAGGTTT	GCCTGGAATG	2250
CACACCAAGG	GCCCCACCCG	CCCAGAACAA	ATGGGACTCC	AGAGGGCCTG	2300
GCCTCACCCCT	CCCTATTCTC	AGTCCTGCAG	CCTGAGCATG	TGCTGGCCGG	2350
CTGTACCCTG	AGGTGCCCTC	CCACTTCCTC	CTTCAGGTTT	TGAGGGGGAC	2400
AGGCTGACAA	GTAGGACCCG	AGGCACTGGA	GGAGCATTGA	AGGAGAAGAT	2450
CTGTAAGTAA	GCCTTTGTCA	GAGCCTCCAA	GGTTCAGTTC	AGTTCTCACC	2500
TAAGGCCTCA	CACACGCTCC	TTCTCTCCCC	AGGCCTGTGG	GTCTTCATTG	2550
CCCAGCTCCT	GCCCGCACTC	CTGCCTGCTG	CCCTGACCAG	AGTCATC	2597
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	2639
GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG GTG	GGT GCG	2681
CAG GCT CCT	GCT ACT GAG	GAG CAG CAG	ACC GCT TCT	TCC TCT	2723

TCT ACT CTA GTG GAA GTT ACC CTG GGG GAG GTG CCT GCT GCC 2765
 GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC 2807
 TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT 2849
 GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATG TTT 2891
 CCC GAG CTG GAG TCC GAG TTC CAA GCA GCA ATC AGT AGG AAG 2933
 ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 2975
 AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGT GTC CTC 3017
 AGA AAT TGG CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC 3059
 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTG GAA 3101
 GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG 3143
 GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG 3185
 CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA 3227
 ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG 3269
 CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG GAC AGT GTC 3311
 TTC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG 3353
 GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT 3395
 GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA 3437
 ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT 3479
 GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT 3521
 TTG AGA GAG GGA GAA GAG TGA 3542
 GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT 3592
 GCACCTTCCA GGGCCCCATC CATTAGCTTC GACTGCCTCG TGTGATATGA 3642
 GGCCCATTC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG 3692
 TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742
 TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792
 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842
 TAAGAGTCCT GTTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG 3892
 TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG 3942
 AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT 3992
 TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT 4042
 TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCCTG 4092
 TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGS 4142
 CCTGGTAGTA GTGGG 4157

- (2) INFORMATION FOR SEQUENCE ID NO: 10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 662 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-21 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATCCCCAT GGATCCAGGA AGAATCCAGT TCCACCCCTG CTGTGAACCC 50
 AGGGAAGTCA CGGGGCCGGA TGTGACGCCA CTGACTTGCG CGTTGGAGGT 100
 CAGAGAACAG CGAGATTCTC GCCCTGAGCA ACGGCCTGAC GTCGGCGGAG 150
 GGAAGCAGGC GCAGGCTCCG TGAGGAGGCA AGGTAAGATG CCGAGGGAGG 200
 ACTGAGGCGG GCCTCACCCC AGACAGAGGG CCCCCAATAA TCCAGCGCTG 250
 CCTCTGCTGC CAGGCCTGGA CCACCCTGCA GGGGAAGACT TCTCAGGCTC 300
 AGTCGCCACC ACCTCACCCC GCCACCCCCC GCCGCTTTAA CCGCAGGGAA 350
 CTCTGGTGTA AGAGCTTTGT GTGACCAGGG CAGGGCTGGT TAGAAGTGCT 400
 CAGGGCCCAG ACTCAGCCAG GAATCAAGGT CAGGACCCCA AGAGGGGACT 450
 GAGGGTAACC CCCCCGCACC CCCACCACCA TTCCCATCCC CCAACACCAA 500
 CCCCACCCCC ATCCCCCAAC ACCAAACCCA CCACCATCGC TAAACATCA 550
 ACGGCACCCC CAAACCCCGA TTCCCATCCC CACCCATCCT GGCAGAATCG 600
 GAGCTTTGCC CCTGCAATCA ACCCACGGAA GCTCCGGGAA TGGCGGCCAA 650
 GCACGCGGAT CC 662

- (2) INFORMATION FOR SEQUENCE ID NO: 11:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1640 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA to mRNA
 (ix) FEATURE:
 (A) NAME/KEY: cDNA MAGE-3
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Sub
D

12

GCCGCGAGGG	AAGCCGGCCC	AGGCTCGGTG	AGGAGGCAAG	GTTCTGAGGG	50
GACAGGCTGA	CCTGGAGGAC	CAGAGGCCCC	CGGAGGAGCA	CTGAAGGAGA	100
AGATCTGCCA	GTGGGTCTCC	ATTGCCCAGC	TCCTGCCCAC	ACTCCCGCCT	150
GTTGCCCTGA	CCAGAGTCAT	C			171
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	213
GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG	GTG GGT GCG	255
CAG GCT CCT	GCT ACT GAG	GAG CAG GAG	GCT GCC TCC	TCC TCT	297
TCT ACT CTA	GTT GAA GTC	ACC CTG GGG	GAG GTG CCT	GCT GCC	339
GAG TCA CCA	GAT CCT CCC	CAG AGT CCT	CAG GGA GCC	TCC AGC	381
CTC CCC ACT	ACC ATG AAC	TAC CCT CTC	TGG AGC CAA	TCC TAT	423
GAG GAC TCC	AGC AAC CAA	GAA GAG GAG	GGG CCA AGC	ACC TTC	465
CCT GAC CTG	GAG TCC GAG	TTC CAA GCA	GCA CTC AGT	AGG AAG	507
GTG GCC GAG	TTG GTT CAT	TTT CTG CTC	CTC AAG TAT	CGA GCC	549
AGG GAG CCG	GTC ACA AAG	GCA GAA ATG	CTG GGG AGT	GTC GTC	591
GGA AAT TGG	CAG TAT TTC	TTT CCT GTG	ATC TTC AGC	AAA GCT	633
TCC AGT TCC	TTG CAG CTG	GTC TTT GGC	ATC GAG CTG	ATG GAA	675
GTG GAC CCC	ATC GGC CAC	TTG TAC ATC	TTT GCC ACC	TGC CTG	717
GGC CTC TCC	TAC GAT GGC	CTG CTG GGT	GAC AAT CAG	ATC ATG	759
CCC AAG GCA	GGC CTC CTG	ATA ATC GTC	CTG GCC ATA	ATC GCA	801
AGA GAG GGC	GAC TGT GCC	CCT GAG GAG	AAA ATC TGG	GAG GAG	843
CTG AGT GTG	TTA GAG GTG	TTT GAG GGG	AGG GAA GAC	AGT ATG	885
TTG GGG GAT	CCC AAG AAG	CTG CTC ACC	CAA CAT TTC	GTG CAG	927
GAA AAC TAC	CTG GAG TAC	CGG CAG GTC	CCC GGC AGT	GAT CCT	969
GCA TGT TAT	GAA TTC CTG	TGG GGT CCA	AGG GCC CTC	GTT GAA	1011
ACC AGC TAT	GTG AAA GTC	CTG CAC CAT	ATG GTA AAG	ATC AGT	1053
GGA GGA CCT	CAC ATT TCC	TAC CCA CCC	CTG CAT GAG	TGG GTT	1095
TTG AGA GAG	GGG GAA GAG	TGA			1116
GTCTGAGCAC	GAGTTGCAGC	CAGGGCCAGT	GGGAGGGGGT	CTGGGCCAGT	1166
GCACCTTCCG	GGGCCGCATC	CCTTAGTTTC	CACAGCCTCC	TGTGACGTGA	1216
GGCCCATCTT	TCACCTTTTG	AAGCGAGCAG	TCAGCATTCT	TAGTAGTGGG	1266
TTTCTGTTCT	GTTGGATGAC	TTTGAGATTA	TTCTTTGTTT	CCTGTTGGAG	1316
TTGTTCAAAT	GTTCCTTTTA	ACGGATGGTT	GAATGAGGGT	CAGCATCCAG	1366
GTTTATGAAT	GACAGTAGTC	ACACATAGTG	CTGTTTATAT	AGTTTAGGAG	1416
TAAGAGTCTT	GttTTTTACT	CAAATTgGGA	AATCCATTCC	ATTTTGTGAA	1466
TTGTGACATA	ATAATAGCAG	TGGTAAAAGT	ATTTGCTTAA	AATTGTGAGC	1516
GAATTAGCAA	TAACATACAT	GAGATAACTC	AAGAAATCAA	AAGATAGTTG	1566
ATTCTTGCCT	TGTACCTCAA	TCTATTCTGT	AAAATTAAAC	AAATATGCAA	1616
ACCAGGATTT	CCTTGACTTC	TTTG			1640

- (2) INFORMATION FOR SEQUENCE ID NO: 12:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 943 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-31 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGATCCTCCA CCCCACTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT 50
 CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG 100
 GCGCGTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG 150
 AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGCTCA 200
 GATAGTGCCA ACGGTGAAGG TTGCCTTGG ATTCAAACCA AGGGCCCCAC 250
 CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT 300
 TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC 350
 CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC 400
 AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG 450
 TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCTCACATGC 500
 TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCCAGCT CCTGCCCA 550
 CTCCCGCCTG TTGCCCTGAC CAGAGTCATC 580
 ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA 622
 GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG 664
 CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT 706
 TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC 748
 GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC 790
 CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT 832
 GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC 874
 CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG 916
 GTG GCC AAG TTG GTT CAT TTT CTG CTC 943

- (2) INFORMATION FOR SEQUENCE ID NO: 13:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2531 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-4 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG 50
 GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC 100
 TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG 150
 GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT 200
 TGGTCTGAGA CAGTGTCTCT AGGTTACAGA GCAGAGGATG CACAGGCTGT 250
 GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA 300
 CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT 350
 CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA 400
 CTTCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC 450
 TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT 500
 TAGAGCCTCT AAGATTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC 550
 TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACCTTG 600
 CCTGCTGCCC TGACCAGAGT CATC 624
 ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 666
 GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCA 708
 CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC 750
 TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT 792
 GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT 834
 GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC 876
 AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC 918
 TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC 960
 AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA 1002
 GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC 1044
 ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA 1086
 GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG 1128
 GAA GTG GAC CCC GCC AGC AAC ACC TAC ACC CTT GTC ACC TGC 1170
 CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC 1212
 TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT 1254
 GCA ATG GAG GGC GAC AGC GGC TCT GAG GAG GAA ATC TGG GAG 1296
 GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT 1338
 GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG 1380
 CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT 1422
 CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT 1464
 GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC 1506
 AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA 1548
 GCT TTG TTA GAG GAG GAA GGA GTC TGA 1578
 GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC 1628
 ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC 1678
 CATTCTTCAC TCTGTTTGAA GAAATAGTC AGTGTCTTA GTAGTGGGT 1728
 TCTATTTTGT TGGATGACTT GGAGATTAT CTCTGTTTCC TTTTACAATT 1778
 GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACCTCA GCATCCAAGT 1828
 TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG 1878
 AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG 1928
 GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT 1978
 GAAATAGGTG AGATAAATTA AAAGATACTT AATCCCCGCC TTATGCCTCA 2028
 GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCTTTGG 2078
 CTTCTGTAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTGA 2128
 ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGGAAGGCC 2178
 AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA 2228
 GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT 2278
 CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT 2328
 GAGAGTGGTC GGGTGTAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA 2378
 AACTGCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC 2428
 AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC 2478

TCTGAGCAGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT
GGG

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2531

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D.

1/2

- (2) INFORMATION FOR SEQUENCE ID NO: 14:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2531 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-41 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

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GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG 50
 GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC 100
 TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG 150
 GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT 200
 TGGTCTGAGA CAGTGTCTCTC AGGTACAGA GCAGAGGATG CACAGGCTGT 250
 GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA 300
 CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT 350
 CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA 400
 CTTCTCTCCT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC 450
 TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT 500
 TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC 550
 TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACCTTGT 600
 CCTGCTGCCC TGAGCAGAGT CATC 624
 ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 666
 GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCG 708
 CAG GCT CCT ACT ACT GAG GAG CAG GCT GCT GTC TCC TCC 750
 TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT 792
 GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT 834
 GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC 876
 AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC 918
 TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC 960
 AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA 1002
 GCC AAG GAG CTG GTC ACA AAG GAA GAA ATG CTG GAG AGA GTC 1044
 ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA 1086
 GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG 1128
 GAA GTG GAC CCC ACC AGC AAC ACC TAC ACC CTT GTC ACC TGC 1170
 CTG GGC CTT CCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC 1212
 TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT 1254
 GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG 1296
 GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT 1338
 GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG 1380
 CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT 1422
 CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT 1464
 GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC 1506
 AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA 1548
 GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA 1578
 GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC 1628
 ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC 1678
 CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT 1728
 TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT 1778
 GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACCTCA GCATCCAAGT 1828
 TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG 1878
 AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG 1928
 GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT 1978
 GAAATAGGTG AGATAAATTA AAAGATACTT AATTCGCCCTA TTATGCCTCA 2028
 GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCTCTGG 2078
 CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTGA 2128
 ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC 2178
 AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA 2228
 GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT 2278
 CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT 2328
 GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA 2378
 AACTCCATTT TCTTCTGAGG GATCTGATTG TAATGAAGCT TGGTGGGTCC 2428

AGGGCCAGAT TCTGAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC
TCTGAGCGGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT
GGG

2478
2528
2531

Sub
D

(2) INFORMATION FOR SEQUENCE ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1068 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

(A) NAME/KEY: cDNA MAGE-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

G GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA 40
 GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG 82
 CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA 124
 ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT 166
 GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT 208
 GGC ATT GAC GTG AAG GAA GTG GAG CCC GCC AGC AAC ACC TAC 250
 ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG 292
 GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC 334
 GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG 376
 GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT 418
 GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC 460
 ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG 502
 GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT 544
 CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG 586
 CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA 628
 TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC 670
 TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGACAG 720
 TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG 770
 GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTT TTAGTAGTGG 820
 GTTTCTATTT TGTGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA 870
 ATTGTTGAAA TGTTCTTTT AATGGATGGT TGAATTAAT TCAGCATCCA 920
 AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT 970
 AAGAGTCTTG TTTTATTTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT 1020
 TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC 1068

- (2) INFORMATION FOR SEQUENCE ID NO: 16:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2226 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-5 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG 50
 GGGACCATTG ACCCCAAGAG GGTGGAGACC TCACAGATTG CAGCCTACCC 100
 TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG 150
 GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT 200
 TGGTCTGAGG CCGTGCCCTC AGGTACACAGA GCAGAGGAGA TGCAGACGTC 250
 TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC 300
 GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG 350
 TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT 400
 CTCACCTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG 450
 GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG 500
 ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCACT TTTTAGCTGA 550
 GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC 600
 AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC 644
 ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 684
 CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG 728
 GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA 770
 TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA 812
 AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC 854
 CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG 896
 TGG CTG ACT TGA 908
 TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCTGGT CACAAAGGCA 958
 GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT 1008
 CTTCCGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA 1058
 AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA 1108
 CTCCTATGAT GGCCTGCTGG TTGATAATAA TCAGATCATG CCCAAGACGG 1158
 GCCTCCTGAT AATCGTCTTG GGCATGATTC CAATGGAGGG CAAATGCGTC 1208
 CCTGAGGAGA AAATCTGGGA GGAGCTGAGT GTGATGAAGG TGTATGTTGG 1258
 GAGGGAGCAC AGTGTCTGTG GGGAGCCCAG GAAGCTGCTC ACCCAAGATT 1308
 TGGTGCAGGA AAATACCTG GAGTACCGGC AGGTGCCCAG CAGTGATCCC 1358
 ATATGCTATG AGTTACTGTG GGGTCCAAGG GCACTCGCTG CTTGAAAGTA 1408
 CTGGAGCACG TGGTCAGGGT CAATGCAAGA GTTCTCATT TCTACCCATC 1458
 CCTGCGTGAA GCAGCTTTGA GAGAGGAGGA AGAGGGAGTC TGAGCATGAG 1508
 CTGCAGCCAG GGCCACTGCG AGGGGGGCTG GGCCAGTGCA CCTTCCAGGG 1558
 CTCCGTCCAG TAGTTTCCCC TGCCTTAATG TGACATGAGG CCCATTCTTC 1608
 TCTCTTTGAA GAGAGCAGTC AACATTCTTA GTAGTGGGT TCTGTTCTAT 1658
 TGGATGACTT TGAGATTTGT CTTTGTTTCC TTTTGGAATT GTTCAAATGT 1708
 TTCTTTTAAT GGGTGGTTGA ATGAACCTCA GCATTCAAAT TTATGAATGA 1758
 CAGTAGTCAC ACATAGTGCT GTTTATATAG TTTAGGAGTA AGAGTCTTGT 1808
 TTTTATTCA GATTGGGAAA TCCATTCCAT TTTGTGAATT GGGACATAGT 1858
 TACAGCAGTG GAATAAGTAT TCATTTAGAA ATGTGAATGA GCAGTAAAC 1908
 TGATGACATA AAGAAATTAA AAGATATTTA ATTCTTGCTT ATACTCAGTC 1958
 TATTCGGTAA AATTTTTTTT AAAAAATGTG CATACCTGGA TTTCCTTGGC 2008
 TTCTTTGAGA ATGTAAGACA AATTAAATCT GAATAAATCA TTCTCCCTGT 2058
 TCACTGGCTC ATTTATTCTC TATGCACTGA GCATTGCTC TGTGGAAGGC 2108
 CCTGGGTTAA TAGTGGAGAT GCTAAGGTAA GCCAGACTCA CCCCTACCCA 2158
 CAGGGTAGTA AAGTCTAGGA GCAGCAGTCA TATAATTAAG GTGGAGAGAT 2208
 GCCCTCTAAG ATGTAGAG 2226

- (2) INFORMATION FOR SEQUENCE ID NO: 17:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2305 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-51 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG 50
 GGGACCATT CACCAAGAG GGTGGAGACC TCACAGATT CAGCCTACCC 100
 TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG 150
 GGCCCATGCA TTCTCTTCC AGGAGCTCCA GGAACAGAC ACTGAGGCCT 200
 TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC 250
 TAGTGCCAGC AGTGACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC 300
 GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG 350
 TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT 400
 CTCACCTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG 450
 GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG 500
 ATCTGTAAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCACT TTTTAGCTGA 550
 GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC 600
 AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC 644
 ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 686
 GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG TGG GTG TGC 728
 AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT CCT CCT CCT 770
 CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG 812
 GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA 854
 TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA 896
 AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC 938
 CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG 980
 TGG CTG ACT TGA 992
 TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCCGGT CACAAAGGCA 1042
 GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT 1092
 CTTCCGGCAA GCCTCCGAGT CCTTCAGCT GGTCTTTGGC ATTGACGTGA 1142
 AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA 1192
 CTCCTATGAT GGCCTGGTGG TTTAATCAGA TCATGCCCAA GACGGGCCCTC 1242
 CTGATAATCG TCTTGGGCAT GATTGCAATG GAGGCAAAAT GCGTCCCTGA 1292
 GGAGAAAATC TGGGAGGAGC TGGGTGTGAT GAAGGTGTAT GTTGGGAGGG 1342
 AGCACAGTGT CTGTGGGGAG CCCAGGAAGC TGCTCACCCA AGATTGTTG 1392
 CAGGAAACT ACCTGGAGTA CCGCAGGTGC CCAGCAGTGA TCCCATATGC 1442
 TATGAGTTAC TGTGGGGTCC AAGGGCACTC GCTGCTTGAA AGTACTGGAG 1492
 CACGTGGTCA GGGTCAATGC AAGAGTTCTC ATTTCCCTACC CATCCCTGCA 1542
 TGAAGCAGCT TTGAGAGAGG AGGAAGAGGG AGTCTGAGCA TGAGCTGCAG 1592
 CCAGGGCCAC TGCAGGGGGG GCTGGGCCAG TGCACCTTCC AGGGCTCCGT 1642
 CCAGTAGTTT CCCCTGCCTT AATGTGACAT GAGGCCCATT CTTCTCTCTT 1692
 TGAAGAGAGC AGTCAACATT CTTAGTAGTG GGTTTCTGTT CTATTGGATG 1742
 ACTTTGAGAT TTGTCTTTGT TTCCTTTTGG AATTGTTCAA ATGTTCTTTT 1792
 TAATGGGTGG TTGAATGAAC TTCAGCATT CAAATTTATGA ATGACAGTAG 1842
 TCACACATAG TGCTGTTTAT ATAGTTTAGG AGTAAGAGTC TTGTTTTTTA 1892
 TTCAGATTGG GAAATCCATT CCATTTTGTG AATTGGGACA TAGTTACAGC 1942
 AGTGGAATAA GTATTCAAT AGAAATGTGA ATGAGCAGTA AAAGTATGA 1992
 GATAAAGAAA TTAAAGATA TTTAATTCTT GCCTTATACT CAGTCTATTC 2042
 GGTAATAATTT TTTTAAATA ATGTGCATAC CTGGATTTC TGGCTTCTT 2092
 TGAGAATGTA AGACAAATTA AATCTGAATA AATCATTCTC CCTGTTCACT 2142
 GGCTCATTTA TTCTCTATGC ACTGAGCATT TGCTCTGTGG AAGGCCCTGG 2192
 GTTAATAGTG GAGATGCTAA GGTAAGCCAG ACTCACCCCT ACCCACAGGG 2242
 TAGTAAAGTC TAGGAGCAGC AGTCATATAA TTAAGGTGGA GAGATGCCCT 2292
 CTAAGATGTA GAG 2305

- (2) INFORMATION FOR SEQUENCE ID NO: 18:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:
 (A) NAME/KEY: MAGE-6 gene
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG 42
CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC 84
GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC 126
GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC 168
TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC 210
TGT GCC CCT GAG GAG 225

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- (2) INFORMATION FOR SEQUENCE ID NO: 19:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1947 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-7 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGAATGGACA ACAAGGGCCC CACACTCCCC AGAACACAAG GGACTCCAGA 50
 GAGCCCAGCC TCACCTTCCC TACTGTCAGT CCTGCAGCCT CAGCCTCTGC 100
 TGGCCGGCTG TACCCTGAGG TGCCCTCTCA CTTCCTCCTT CAGGTTCTCA 150
 GCGGACAGGC CGGCCAGGAG GTCAGAAGCC CCAGGAGGCC CCAGAGGAGC 200
 ACCGAAGGAG AAGATCTGTA AGTAGGCCTT TGTTAGGGCC TCCAGGGCGT 250
 GGTTCACAAA TGAGGCCCCC CACAAGCTCC TTCTCTCCCC AGATCTGTGG 300
 GTTCCTCCCC ATCGCGCAGC TGCTGCCCCG ACTCCAGCCT GCTGCCCTGA 350
 CCAGAGTCAT CATGTCTTCT GAGCAGAGGA GTCAGCACTG CAAGCCTGAG 400
 GATGCCTTGA GGCCCAAGGA CAGGAGGCTC TGGGCCTGGT GGGTGCAGCAG 450
 GCTCCCGCCA CCGAGGAGGA CGAGGCTGCC TCCTCCTTCA CTCTGATTGA 500
 AGGCACCCCT GAGGAGGTGG CTGCTGCTGG GTCCCCAGT CCTCCCCTGA 550
 GTCTCAGGGT TCCTCCTTTT CCCTGACCAT CAGCAACAAC ACTCTATGGA 600
 GCCAATCCAG TGAGGGCACC AGCAGCCGGG AAGAGGAGGG GCCAACCACC 650
 TAGACACACC CCGCTCACCT GGCGTCCTTG TTCCA 685
 ATG GGA AGG TGG CTG AGT TGG TTC GCT TCC TGC TGC ACA AGT 727
 ATC GAG TCA AGG AGC TGG TCA CAA AGG CAG AAA TGC TGG ACA 769
 GTG TCA TCA AAA ATT ACA AGC ACT AGT TTC CTT GTG ATC TAT 811
 GGC AAA GCC TCA GAG TGC ATG CAG GTG ATG TTT GGC ATT GAC 853
 ATG AAG GAA GTG GAC CCC GCG GCC ACT CCT ACG TCC TTG TCA 895
 CCT GCT TGG GCC TCT CCT ACA ATG GCC TGC TGG GTG ATG ATC 937
 AGA GCA TGC CCG AGA CCG GCC TTC TGA 964
 TTATGGTCTT GACCATGATC TTAATGGAGG GCCACTGTGC CCCTGAGGAG 1014
 GCAATCTGGG AAGCGTTGAG TGTAATGGTG TATGATGGGA TGGAGCAGTT 1064
 TCTTTGGGCA GCTGAGGAAG CTGCTCACCC AAGATTGGGT GCAGGAAAAC 1114
 TACCTGCAAT ACCGCCAGGT GCCCAGCAGT GATCCCCCGT GCTACCACTT 1164
 CCTGTGGGGT CCAAGGGCCC TCATTGAAAC CAGCTATGTG AAAGTCCTGG 1214
 AGTATGCAGC CAGGGTCAGT ACTAAAGAGA GCATTTCCTA CCCATCCCTG 1264
 CATGAAGAGG CTTTGGGAGA GGAGGAAGAG GGAGTCTGAG CAGAAGTTGC 1314
 AGCCAGGGCC AGTGGGGCAG ATTGGGGGAG GGCCTGGGCA GTGCACGTTT 1364
 CACACATCCA CCACCTTCCC TGTCTGTGTA CATGAGGCCG ATTCTTCACT 1414
 CTGTGTTTGA AGAGAGCAGT CAATGTTCTC AGTAGCGGGG AGTGTGTTGG 1464
 GTGTGAGGGA ATACAAGGTG GACCATCTCT CAGTTCTCTG TCTCTGGGC 1514
 GATTTGGAGG TTTATCTTTG TTTCTTTTGG CAGTCGTTCA AATGTTCTCT 1564
 TTAATGGATG GTGTAATGAA CTTCAACATT CATTTTCATG ATGACAGTAG 1614
 GCAGACTTAC TGTTTTTTAT ATAGTTAAAA GTAAGTGCAT TGTTTTTTAT 1664
 TTATGTAAGA AAATCTATGT TATTTCTTGA ATTGGGACAA CATAACATAG 1714
 CAGAGGATTA AGTACCTTTT ATAATGTGAA AGAACAAAGC GGTAAAAATG 1764
 GTGAGATAAA GAAATAAAGA AATTAAATTG GCTGGGCACG GTGGCTCAGG 1814
 CCTGTAATCC CAGCACTTTA GGAGGCAGAG GCACGGGGAT CACGAGGTCA 1864
 GGAGATCGAG ACCATTCTGG CTAACACAGT GAAACACCAT CTCTATTAAA 1914
 AATACAAAAC TTAGCCGGGC GTGGTGGCGG GTG 1947

- (2) INFORMATION FOR SEQUENCE ID NO: 20:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1810 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-8 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GAGCTCCAGG AACGAGGCTG TGAGGTCTTG GTCTGAGGCA GTATCTTCAA 50
 TCACAGAGCA TAAGAGGCCG AGGCAGTAGT AGCAGTCAAG CTGAGGTGGT 100
 GTTTCCCCTG TATGTATACC AGAGGCCCTT CTGGCATCAG AACAGCAGGA 150
 ACCCCACAGT TCCTGGGCTT ACCAGCCCTT TTGTCACTCC TGGAGCCTTG 200
 GCCTTTGCCA GGAGGCTGCA CCCTGAGATG CCCTCTCAAT TTCTCCTTCA 250
 GGTTCGCAGA GAACAGGCCA GCCAGGAGGT CAGGAGGCCC CAGAGAAGCA 300
 CTGAAGAAGA CCTGTAAGTA GACCTTTGTT AGGGCATCCA GGGTGTAGTA 350
 CCCAGCTGAG GCCTCTCACA CGCTTCCTCT CTCCCCAGGC CTGTGGGTCT 400
 CAATTGCCCA GCTCCGGCCC AACTCTCCT GCTGCCCTGA CCTGAGTCAT 450
 C 451
 ATG CTT CTT GGG CAG AAG AGT CAG CGC TAC AAG GCT GAG GAA 493
 GGC CTT CAG GCC CAA GGA GAG GCA CCA GGG CTT ATG GAT GTG 535
 CAG ATT CCC ACA GCT GAG GAG CAG AAG GCT GCA TCC TCC TCC 577
 TCT ACT CTG ATC ATG GGA ACC CTT GAG GAG GTG ACT GAT TCT 619
 GGG TCA CCA AGT CCT CCC CAG AGT CCT GAG GGT GCC TCC TCT 661
 TCC CTG ACT GTC ACC GAC AGC ACT CTG TGG AGC CAA TCC GAT 703
 GAG GGT TCC AGC AGC AAT GAA GAG GAG GGG CCA AGC ACC TCC 745
 CCG GAC CCA GCT CAC CTG GAG TCC CTG TTC CGG GAA GCA CTT 787
 GAT GAG AAA GTG GCT GAG TTA GTT CGT TTC CTG CTC CGC AAA 829
 TAT CAA ATT AAG GAG CCG GTC ACA AAG GCA GAA ATG CTT GAG 871
 AGT GTC ATC AAA AAT TAC AAG AAC CAC TTT CCT GAT ATC TTC 913
 AGC AAA GCC TCT GAG TGC ATG CAG GTG ATC TTT GGC ATT GAT 955
 GTG AAG GAA GTG GAC CCT GCC GGC CAC TCC TAC ATC CTT GTC 997
 ACC TGC CTG GGC CTC TCC TAT GAT GGC CTG CTG GGT GAT GAT 1039
 CAG AGT ACG CCC AAG ACC GGC CTC CTG ATA ATC GTC CTG GGC 1081
 ATG ATC TTA ATG GAG GGC AGC CGC GCC CCG GAG GAG GCA ATC 1123
 TGG GAA GCA TTG AGT GTG ATG GGG GCT GTA TGA 1156
 TGGGAGGGAG CACAGTGTCT ATTGGAAGCT CAGGAAGCTG CTCACCCAAG 1206
 AGTGGGTGCA GGAGAACTAC CTGGAGTACC GCCAGGCGCC CGGCAGTGAT 1256
 CCTGTGCGCT ACGAGTTCCT GTGGGGTCCA AGGGCCCTTG CTGAAACCAG 1306
 CTATGTGAAA GTCCTGGAGC ATGTGGTCAG GGTCAATGCA AGAGTTCGCA 1356
 TTTCTACCC ATCCCTGCAT GAAGAGGCTT TGGGAGAGGA GAAAGGAGTT 1406
 TGAGCAGGAG TTGCAGCTAG GGCCAGTGGG GCAGGTTGTG GGAGGGCCTG 1456
 GGCCAGTGCA CGTTCCAGGG CCACATCCAC CACTTCCCT GCTCTGTTAC 1506
 ATGAGGCCCA TTCTTCACTC TGTGTTTGAA GAGAGCAGTC ACAGTTCTCA 1556
 GTAGTGGGGA GCATGTTGGG TGTGAGGGAA CACAGTGTGG ACCATCTCTC 1606
 AGTTCTCTGT CTATTGGGCG ATTTGGAGGT TTATCTTTGT TTCCTTTTGG 1656
 AATTGTTCCA ATGTTCTTTC TAATGGATGG TGTAATGAAC TTCAACATTC 1706
 ATTTTATGTA TGACAGTAGA CAGACTTACT GCTTTTATA TAGTTTAGGA 1756
 GTAAGAGTCT TGCTTTTCAT TTATACTGGG AAACCCATGT TATTTCTTGA 1806
 ATTC 1810

- (2) INFORMATION FOR SEQUENCE ID NO: 21:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1412 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-9 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TCTGAGACAG TGTCCTCAGG TCGCAGAGCA GAGGAGACCC AGGCAGTGTC 50
 AGCAGTGAAG GTGAAGTGTT CACCCTGAAT GTGCACCAAG GGCCCCACCT 100
 GCCCCAGCAC ACATGGGACC CCATAGCACC TGGCCCCATT CCCCCTACTG 150
 TCACTCATAG AGCCTTGATC TCTGCAGGCT AGCTGCACGC TGAGTAGCCC 200
 TCTCACTTCC TCCCTCAGGT TCTCGGGACA GGCTAACCAG GAGGACAGGA 250
 GCCCCAAGAG GCCCCAGAGC AGCACTGACG AAGACCTGTA AGTCAGCCTT 300
 TGTTAGAACC TCCAAGGTTT GGTCTCAGC TGAAGTCTCT CACACACTCC 350
 CTCTCTCCCC AGGCCTGTGG GTCTCCATCG CCCAGCTCCT GCCCACGCTC 400
 CTGACTGCTG CCCTGACCAG AGTCATC 427
 ATG TCT CTC GAG CAG AGG AGT CCG CAC TGC AAG CCT GAT GAA 469
 GAC CTT GAA GCC CAA GGA GAG GAC TTG GGC CTG ATG GGT GCA 511
 CAG GAA CCC ACA GGC GAG GAG GAG GAG ACT ACC TCC TCC TCT 553
 GAC AGC AAG GAG GAG GAG GTG TCT GCT GCT GGG TCA TCA AGT 595
 CCT CCC CAG AGT CCT CAG GGA GGC GCT TCC TCC TCC ATT TCC 637
 GTC TAC TAC ACT TTA TGG AGC CAA TTC GAT GAG GGC TCC AGC 679
 AGT CAA GAA GAG GAA GAG CCA AGC TCC TGG GTC GAC CCA GCT 721
 CAG CTG GAG TTC ATG TTC CAA GAA GCA CTG AAA TTG AAG GTG 763
 GCT GAG TTG GTT CAT TTC CTG CTC CAC AAA TAT CGA GTC AAG 805
 GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGC GTC ATC AAA 847
 AAT TAC AAG CGC TAC TTT CCT GTG ATC TTC GGC AAA GCC TCC 889
 GAG TTC ATG CAG GTG ATC TTT GGC ACT GAT GTG AAG GAG GTG 931
 GAC CCC GCC GGC CAC TCC TAC ATC CTT GTC ACT GGT CTT GGC 973
 CTC TCG TGC GAT AGC ATG CTG GGT GAT GGT CAT AGC ATG CCC 1015
 AAG GCC GCC CTC CTG ATC ATT GTC CTG GGT GTG ATC GTA ACC 1057
 AAA GAC AAC TGC GCC CCT GAA GAG GTT ATC TGG GAA GCG TTG 1099
 AGT GTG ATG GGG GTG TAT GTT GGG AAG GAG CAC ATG TTC TAC 1141
 GGG GAG CCC AGG AAG CTG CTC ACC CAA GAT TGG GTG CAG GAA 1183
 AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCG 1225
 CAC TAC GAG TTC CTG TGG GGT TCC AAG GCC CAC GCT GAA ACC 1267
 AGC TAT GAG AAG GTC ATA AAT TAT TTG GTC ATG CTC AAT GCA 1309
 AGA GAG CCC ATC TGC TAC CCA TCC CTT TAT GAA GAG GTT TTG 1351
 GGA GAG GAG CAA GAG GGA GTC TGA 1375
 GCACCAGCCG CAGCCGGGCG CAAAGTTTGT GGGGTCA 1412

- (x) INFORMATION FOR SEQUENCE ID NO: 22:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 920 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-10 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Sub
D-1

1
C

ACCTGCTCCA	GGACAAAGTG	GACCCCACTG	CATCAGCTCC	ACCTACCCTA	50
CTGTCAGTCC	TGGAGCCTTG	GCCTCTGCCG	GCTGCATCCT	GAGGAGCCAT	100
CTCTCACTTC	CTTCTTCAGG	TTCTCAGGGG	ACAGGGAGAG	CAAGAGGTCA	150
AGAGCTGTGG	GACACCACAG	AGCAGCACTG	AAGGAGAAGA	CCTGTAAGTT	200
GGCCTTTGTT	AGAACCTCCA	GGGTGTGGTT	CTCAGCTGTG	GCCACTTACA	250
CCCTCCCTCT	CTCCCCAGGC	CTGTGGGTCC	CCATCGCCCA	AGTCCTGCCC	300
ACACTCCCAC	CTGCTACCCT	GATCAGAGTC	ATC		333
ATG CCT CGA	GCT CCA AAG	CGT CAG CGC	TGC ATG CCT	GAA GAA	375
GAT CTT CAA	TCC CAA AGT	GAG ACA CAG	GGC CTC GAG	GGT GCA	417
CAG GCT CCC	CTG GCT GTG	GAG GAG GAT	GCT TCA TCA	TCC ACT	459
TCC ACC AGC	TCC TCT TTT	CCA TCC TCT	TTT CCC TCC	TCC TCC	501
TCT TCC TCC	TCC TCC TGC	TAT CCT CTA	ATA CCA AGC	ACC	543
CCA GAG GAG	GTT TCT GCT	GAT GAT GAG	ACA CCA AAT	CCT CCC	585
CAG AGT GCT	CAG ATA GCC	TGC TCC TCC	CCC TCG GTC	GTT GCT	627
TCC CTT CCA	TTA GAT CAA	TCT GAT GAG	GGC TCC AGC	AGC CAA	669
AAG GAG GAG	AGT CCA AGC	ACC CTA CAG	GTC CTG CCA	GAC AGT	711
GAG TCT TTA	CCC AGA AGT	GAG ATA GAT	GAA AAG GTG	ACT GAT	753
TTG GTG CAG	TTT CTG CTC	TTC AAG TAT	CAA ATG AAG	GAG CCG	795
ATC ACA AAG	GCA GAA ATA	CTG GAG AGT	GTC ATA AAA	AAT TAT	837
GAA GAC CAC	TTC CCT TTG	TTG TTT AGT	GAA GCC TCC	GAG TGC	879
ATG CTG CTG	GTC TTT GGC	ATT GAT GTA	AAG GAA GTG	GAT CC	920

- (2) INFORMATION FOR SEQUENCE ID NO: 23:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1107 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-11 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Sub D.7

AGAGAACAGG	CCAACCTGGA	GGACAGGAGT	CCCAGGAGAA	CCCAGAGGAT	50
CACTGGAGGA	GAACAAQTGT	AAGTAGGCCT	TTGTTAGATT	CTCCATGGTT	100
CATATCTCAT	CTGAGTCTGT	TCTCACGCTC	CCTCTCTCCC	CAGGCTGTGG	150
GGCCCCATCA	CCCAGATATT	TCCCACAGTT	CGGCCTGCTG	ACCTAACCAG	200
AGTCATCATG	CCTCTTGAGC	AAAGAAGTCA	GCACTGCAAG	CCTGAGGAAG	250
CCTTCAGGCC	CAAGAAGAAG	ACCTGGGCCT	GGTGGGTGCA	CAGGCTCTCC	300
AAGCTGAGGA	GCAGGAGGCT	GCCTTCTTCT	CCTCTACTCT	GAATGTGGGC	350
ACTCTAGAGG	AGTTGCCTGC	TGCTGAGTCA	CCAAGTCCTC	CCCAGAGTCC	400
TCAGGAAGAG	TCCTTCTCTC	CCAATGCCAT	GGATGCCATC	TTTGGGAGCC	450
TATCTGATGA	GGGCTCTGGC	AGCCAAGAAA	AGGAGGGGCC	AAGTACCTCG	500
CCTGACCTGA	TAGACCCTGA	GTCCTTTTCC	CAAGATATAC	TACATGACAA	550
GATAATTGAT	TTGGTTCATT	TATTCTCCGC	AAGTATCGAG	TCAAGGGGCT	600
GATCACAAG	GCAGAA				616
ATG CTG GGG	AGT GTC ATC AAA	AAT TAT GAG GAC	TAC TTT CCT		658
GAG ATA TTT	AGG GAA GCC TCT	GTA TGC ATG CAA	CTG CTC TTT		700
GGC ATT GAT	GTG AAG GAA GTG	GAC CCC ACT AGC	CAC TCC TAT		742
GTC CTT GTC	ACC TCC CTC AAC	CTC TCT TAT GAT	GGC ATA CAG		784
TGT AAT GAG	CAG AGC ATG CCC	AAG TCT GGC CTC	CTG ATA ATA		826
GTC CTG GGT	GTA ATC TTC ATG	GAG GGG AAC TGC	ATC CCT GAA		868
GAG GTT ATG	TGG GAA GTC CTG	AGC ATT ATG GGG	GTG TAT GCT		910
GGA AGG GAG	CAC TTC CTC TTT	GGG GAG CCC AAG	AGG CTC CTT		952
ACC CAA AAT	TGG GTG CAG GAA	AAG TAC CTG GTG	TAC CGG CAG		994
GTG CCC GGC	ACT GAT CCT GCA	TGC TAT GAG TTC	CTG TGG GGT		1036
CCA AGG GCC	CAC GCT GAG ACC	AGC AAG ATG AAA	GTT CTT GAG		1078
TAC ATA GCC	AAT GCC AAT GGG	AGG GAT CC			1107

- (2) INFORMATION FOR SEQUENCE ID NO: 24:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2150 base pairs
- (B) TYPE: nucleic acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (ix) FEATURE:
- (A) NAME/KEY: smage-I
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Sub 517

TCTGTCTGCA	TATGCCTCCA	CTTGTGTGTA	GCAGTCTCAA	ATGGATCTCT	50
CTCTACAGAC	CTCTGTCTGT	GTCTGGCACC	CTAAGTGGCT	TTGCATGGGC	100
ACAGGTTTCT	GCCCCCTGCAT	GGAGCTTAAA	TAGATCTTTC	TCCACAGGCC	150
TATACCCCTG	CATTGTAAGT	TTAAGTGGCT	TTATGTGGAT	ACAGGTCTCT	200
GCCCTTGAT	GCAGGCCTAA	GTTTTCTGT	CTGCTTAACC	CCTCCAAGTG	250
AAGCTAGTGA	AAGATCTAAC	CCACTTTTGG	AAGTCTGAAA	CTAGACTTTT	300
ATGCAGTGGC	CTAACAAGTT	TTAATTTCTT	CCACAGGGTT	TGCAGAAAAG	350
AGCTTGATCC	ACGAGTTTCA	AAGTCCTGGT	ATGTTCTAG	AAAG	394
ATG TTC TCC TGG AAA GCT TCA AAA GCC AGG TCT CCA TTA AGT					436
CCA AGG TAT TCT CTA CCT GGT AGT ACA GAG GTA CTT ACA GGT					478
TGT CAT TCT TAT CCT TCC AGA TTC CTG TCT GCC AGC TCT TTT					520
ACT TCA GCC CTG AGC ACA GTC AAC ATG CCT AGG GGT CAA AAG					565
AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG CAG TCA CGC AGG					604
GAG GTT CCA GTA GTT CAG CCC ACT GCA GAG GAA GCA GGG TCT					646
TCT CCT GTT GAC CAG AGT GCT GGG TCC AGC TTC CCT GGT GGT					688
TCT GCT CCT CAG GGT GTG AAA ACC CCT GGA TCT TTT GGT GCA					730
GGT GTA TCC TGC ACA GGC TCT GGT ATA GGT GGT AGA AAT GCT					772
GCT GTC CTG CCT GAT ACA AAA AGT TCA GAT GGC ACC CAG GCA					814
GGG ACT TCC ATT CAG CAC ACA CTG AAA GAT CCT ATC ATG AGG					856
AAG GCT AGT GTG CTG ATA GAA TTC CTG CTA GAT AAA TTT AAG					898
ATG AAA GAA GCA GTT ACA AGG AGT GAA ATG CTG GCA GTA GTT					940
AAC AAG AAG TAT AAG GAG CAA TTC CCT GAG ATC CTC AGG AGA					982
ACT TCT GCA CGC CTA GAA TTA GTC TTT GGT CTT GAG TTG AAG					1024
GAA ATT GAT CCC AGC ACT CAT TCC TAT TTG CTG GTA GGC AAA					1066
CTG GGT CTT TCC ACT GAG GGA AGT TTG AGT AGT AAC TGG GGG					1108
TTG CCT AGG ACA GGT CTC CTA ATG TCT GTC CTA GGT GTG ATC					1150
TTC ATG AAG GGT AAC CGT GCC ACT GAG CAA GAG GTC TGG CAA					1192
TTT CTG CAT GGA GTG GGG GTA TAT GCT GGG AAG AAG CAC TTG					1234
ATC TTT GGC GAG CCT GAG GAG TTT ATA AGA GAT GTA GTG CGG					1276
GAA AAT TAC CTG GAG TAC CGC CAG GTA CCT GGC AGT GAT CCC					1314
CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA GCC CAT GCT GAA					1360
ACA ACC AAG ATG AAA GTC CTG GAA GTT TTA GCT AAA GTC AAT					1402
GGC ACA GTC CCT AGT GCC TTC CCT AAT CTC TAC CAG TTG GCT					1444
CTT AGA GAT CAG GCA GGA GGG GTG CCA AGA AGG AGA GTT CAA					1486
GGC AAG GGT GTT CAT TCC AAG GCC CCA TCC CAA AAG TCC TCT					1528
AAC ATG TAG					1537
TTGAGTCTGT	TCTGTTGTGT	TTGAAAAACA	GTCAGGCTCC	TAATCAGTAG	1587
AGAGTTTATA	GCCTACCAGA	ACCAACATGC	ATCCATTCTT	GGCCTGTTAT	1637
ACATTAGTAG	AATGGAGGCT	ATTTTGTGTA	CTTTTCAAAT	GTTTGTTTAA	1687
CTAAACAGTG	CTTTTGGCCA	TGCTTCTTGT	TAAGTGCATA	AAGAGGTAAC	1737
TGTCATTGT	CAGATTAGGA	CTTGTTTTGT	TATTTGCAAC	AAACTGGAAA	1787
ACATTATTTT	GTTTTTACTA	AAACATTGTG	TAACATTGCA	TTGGAGAAGG	1837
GATTGTGATG	GCAATGTGAT	ATCATAACAGT	GGTGAAACAA	CAGTGAAGTG	1887
GGAAAGTTTA	TATTGTTAAT	TTTGAAAATT	TTATGAGTGT	GATTGCTGTA	1937
TACTTTTTTC	TTTTTTGTAT	AATGCTAAGT	GAAATAAAGT	TGGATTTGAT	1987
GACTTTACTC	AAATTCATTA	GAAAGTAAAT	CGTAAACTC	TATTACTTTA	2037
TTATTTTCTT	CAATTATGAA	TTAAGCATTG	GTTATCTGGA	AGTTTCTCCA	2087
GTAGCACAGG	ATCTAGTATG	AAATGTATCT	AGTATAGGCA	CTGACAGTGA	2137
GTTATCAGAG	TCT				2150

- (2) INFORMATION FOR SEQUENCE ID NO: 25:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2099 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: smage-II
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Sub D

ACCTTATTGG	GCTGTCTGTC	ATATGCCTCC	ACTTGTGTGT	AGCAGTCTCA	50
AATGGATCTC	TCTCTACAGA	CCTCTGTCTG	TGTCTGGCAC	CCTAAGTGGC	100
TTTGCATGGG	CACAGGTTTC	TGCCCCCTGCA	TGGAGCTTAA	ATAGATCTTT	150
CTCCACAGGC	CTATACCCCT	GCATTGTAAG	TTTAAGTGGC	TTTATGTGGA	200
TACAGGTCTC	TGCCCTTGTA	TGCAGGCCTA	AGTTTTTCTG	TCTGCTTAGC	250
CCCTCCAAGT	GAAGCTAGTG	AAAGATCTAA	CCCACTTTTG	GAAGTCTGAA	300
ACTAGACTTT	TATGCAGTGG	CCTAACAAAGT	TTTAATTTCT	TCCACAGGGT	350
TTGCAGAAAA	GAGCTTGATC	CACGAGTTCG	GAAGTCCTGG	TATGTTCCCTA	400
GAAAGATGTT	CTCCTGGAAA	GCTTCAAAAG	CCAGGTCTCC	ATTAAAGTCCA	450
AGGTATTCTC	TACCTGGTAG	TACAGAGGTA	CTTACAGGTT	GTCATTCTTA	500
TCTTTCCAGA	TTCCTGTCTG	CCAGCTCTTT	TACTTCAGCC	CTGAGCACAG	550
TCAACATGCC	TAGGGGTCAA	AAGAGTAAGA	CCCGCTCCCG	TGCAAAACGA	600
CAGCAGTCAC	GCAGGGAGGT	TCCAGTAGTT	CAGCCCACTG	CAGAGGAAGC	650
AGGGTCTTCT	CCTGTTGACC	AGAGTGCTGG	GTCCAGCTTC	CCTGGTGGTT	700
CTGCTCCTCA	GGGTGTGAAA	ACCCCTGGAT	CTTTTGGTGC	AGGTGTATCC	750
TGCACAGGCT	CTGGTATAGG	TGGTAGAAAT	GCTGCTGTCC	TGCCTGATAC	800
AAAAAGTTCA	GATGGCACCC	AGGCAGGGAC	TTCCATTGAG	CACACACTGA	850
AAGATCCTAT	CATGAGGAAG	GCTAGTGTGC	TGATAGAATT	CCTGCTAGAT	900
AAGTTTAAAG	TGAAAGAAGC	AGTTACAAGG	AGTGAATGAT	TGGCAGTAGT	950
TAACAAGAAG	TATAAGGAGC	AATTCCCTGA	GATCCTCAGG	AGAACTTCTG	1000
CACGCCTAGA	ATTAGTCTTT	GCTCTTGTGT	TGAAGGAAAT	TGATCCCAGC	1050
ACTCATTCTC	ATTTGCTGGT	AGGCAAACCT	GGTCTTTCCA	CTGAGGGAAG	1100
TTTGAGTAGT	AACTGGGGGT	TGCCTAGGAG	AGGTCTCCTA	ATGTCGTGTC	1150
TAGGTGTGAT	CTTCATGAAG	GGTAACCGTG	CCACTGAGCA	AGAGGTCTGG	1200
CAATTTCTGC	ATGGAGTGGG	GGTATATGCT	GGGAAGAAGC	ACTTGATCTT	1250
TGGCGAGCCT	GAGGAGTTTA	TAAGAGATGT	AGTGCGGGAA	AATTACCTGG	1300
AGTACCGCCA	GGTACCTGGC	AGTGATCCCC	CAAGCTATGA	GTTCTGTGTT	1350
GGACCCAGAG	CCCATGCTGA	AACAACCAAG	ATGAAGTCC	TGGAAGTTTT	1400
AGCTAAAGTC	AATGGCACAG	TCCCTAGTGC	CTTCCCTAAT	CTCTACCACT	1450
TGGCTCTTAG	AGATCAGGCA	GGAGGGGTGC	CAAGAAGGAG	AGTTCAAGGC	1500
AAGGGTGTTC	ATTCCAAGGC	CCCATCCCAA	AAGTCCTCTA	ACATGTAGTT	1550
GAGTCTGTTC	TGTTGTGTTT	GAAAAACAGT	CAGGCTCCTA	ATCAGTAGAG	1600
AGTTCATAGC	CTACCAGAAC	CAACATGCAT	CCATTCTTGG	CCTGTTATAC	1650
ATTAGTAGAA	TGGAGGCTAT	TTTTGTTACT	TTTCAAATGT	TTGTTTAACT	1700
AAACAGTGCT	TTTTGCCATG	CTTCTTGTTA	ACTGCATAAA	GAGGTAAGTC	1750
TCACTTGTCA	GATTAGGACT	TGTTTTGTGA	TTTGCAACAA	ACTGGAAAAC	1800
ATTATTTTGT	TTTTACTAAA	ACATTGTGTA	ACATTGCATT	GGAGAAGGGA	1850
TTGTCATGGC	AATGTGATAT	CATACAGTGG	TGAAACAACA	GTGAAGTGGG	1900
AAAGTTTATA	TTGTTAGTTT	TGAAAATTTT	ATGAGTGTGA	TTGCTGTATA	1950
CTTTTTTCTT	TTTTGTATAA	TGCTAAGTGA	AATAAAGTTG	GATTGTATGA	2000
CTTTACTCAA	ATTCATTAGA	AAGTAAATCA	TAAAACCTCT	TTACTTTATT	2050
ATTTTCTTCA	ATTATTAATT	AAGCATTGGT	TATCTGGAAG	TTTCTCCAG	2099

- (2) INFORMATION FOR SEQUENCE ID NO: 26:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acids
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Ala Asp Pro Thr Gly His Ser Tyr
